

Estimation of Variability, Heritability and Genetic Advance Among potato genotypes in (*Solanum tuberosum* L.) in Kellem Wollaga zone

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Abstract

The study was conducted at Haro Sabu Agricultural Research center of Belam sub-site during 2023 main cropping season to estimate the genetic variability, heritability, and genetic advance for 34 potato genotypes and two standard check potato varieties viz Gudanie and Belete. The experiment was laid down 6x6 simple lattice design. The analysis of variance was performed, and the estimation of variance components, heritability in a broad sense, and genetic advance were conducted. The mean squares due to genotypes were highly significant ($P < 0.01$) for days to maturity, marketable and total tuber yield while tuber size, number of tuber per hill and average tuber weight were significant ($P < 0.05$) whereas unmarketable yield was non-significant. In this experiment, genotypic variance values ranged from 0.01 to 27.84 for average tuber weight and total tuber yield, respectively, while phenotypic variance values ranged from 0.03 for total average tuber weight to 40.46 for total tuber yield. The GCV values ranged from 0.04% for marketable yield to 30.60% unmarketable yield, while, the PCV values ranged from 5.24% for days to maturity to 48.67% for unmarketable yield. Estimates of heritability in a broad sense ranged from 39.52% for unmarketable yield to 68.80 for total tuber yield, whereas genetic advance as a percentage of mean ranged from 3.91% for days to maturity to 216.18% for total tuber yield. According to the study results, a high range of variability for most of the investigated traits was observed, indicating a sufficient chance of selecting the best genotypes to improve potato productivity through selection. In the current study, high heritability joined with high- expected genetic advance as a percentage of mean was recorded for marketable yield and total tuber yield, and those characters could be used as good criteria for selection in the potato improvement program.

Keywords— Broad Sense Heritability, Genotypic variance, Phenotypic Coefficient, Potato genotypes

I. INTRODUCTION

Potatoes (*Solanum tuberosum* L.) are the third-largest food crop in the world in terms of human consumption, next to rice and wheat (Lal et al, 2022). Global crop production surpasses 359 million metric tons, and more than a billion people eat potatoes (FAOSTAT, 2022). It was grown over 25 million hectares of land in about 161 different countries (FAOSTAT, 2019).

Ethiopia has an immense potential to boost the productivity of potato (*Solanum tuberosum* L.),

especially in the highlands (Gebremedhin et al., 2013). In Ethiopia potato is the first among root and tuber crops in both area of production and productivity per unit area (CSA 2022). The production of potato was 1,309,566.85 tone on 78478.72 hectares with 16.6t/ha of productivity in Ethiopia. Whereas it production was 47,763.44 tons on area coverage of 42542.38 hectares with productivity of 11.23t/ha in Oromia region (CSA 2022). Oromia shared 54.21% potato production in area coverage however its productivity is very below the

average productivity of potato at national level. This might be due to many factors contributed to low production and productivity, including biotic (disease, insect), abiotic (low soil fertility, poor agronomic management), and failure to use appropriate technology (improved variety, fertilizer) (Oliyad, 2021). Therefore, tailoring a new variety of potato having high yield potential, resistance to disease and adaptable to wide agro-ecological zones through breeding work must be a high priority.

A number of phases were engaged in the systematic breeding process, including the collection of germplasm, the evaluation of genetic variability, the creation of genetic variability, the application of selection, and the promotion of selected genotypes to be released as commercial varieties (Carena, 2021). Genetic diversity in a population is a prerequisite for an effective plant-breeding program. Investigation and a deeper comprehension of the variability are necessary for efficient and effective breeding activities existing in a population base of a crop is required so that it can be exploited by plant breeders for crop improvement. Additionally, the degree of genetic variability in a crop and the quantity of heritable variation from parents to offspring are both important factors in the success of any crop improvement work (Habtamu, 2023).

Knowledge of the genetic parameters, such as heritability and genetic advance, is essential to help guide an effective breeding strategy (Getachew *et al*, 2016). Such information will allow plant breeders to predict the response to the selection of breeding programs (Bulent *et al*, 2013). Estimating genetic coefficient of variation, genetic advance, and broad-sense heritability (h^2) would be useful for plant breeders to execute selection in breeding programs (Johnson *et al*, 1955). Most selection methods would be used high heritability associated with high genetic advance as a clue in most selection programs (Mishra *et al*, 2006).

The degree to which a character may be passed down from parent to offspring is typically assessed using heritability, which is a measure of the genetic link between parent and progeny. It is important for plant breeders because it provides information on the extent to which a particular character can be transmitted from the parent to the progeny (Carena, 2021). Heritability estimates on some important characteristics of potatoes have been carried out by several researchers

(Habtamu, 2023; Gebrehanna *et al*, 2022; Zeleke *et al*, 2021). Similar to this, genetic advance is also essential since it demonstrates the level of improvement in a character that resulted from one cycle of selection. High genetic advance combined with high heritability estimates provides the ideal condition to decide the criteria of selection (Carena, 2021). Therefore, estimating genetic variance aids plant breeders in selecting the most effective breeding strategy for enhancing crops while utilizing available resources.

Genetic variability, which is due to genetic differences among individuals within a population, is the foundation of plant breeding since proper management of diversity can produce a permanent gain in the performance of plants and can safeguard against seasonal fluctuations (Deshmukh *et al*, 1986). Moreover, knowledge on the degree of genetic variability present among genotypes and the association of quantitative characters with yield is vital for any crop improvement program and also to develop suitable selection strategies (Fekadu *et al*, 2013). Such information is insufficient owing to the limited work done by the Ethiopian potato breeding program within the existing genetic pool in the country. So that it is important to study and generate information on genetic variability, genotypic coefficient of variation, heritability, and genetic advance of the potato to estimate the progress of their breeding program in the future. Therefore, the current study was carried out with the objective of estimating the nature and extent of genetic variability, heritability, and genetic advance in yield and yield components among 34 potato genotypes and two standard checks.

II. MATERIAL AND METHODS

2.1. Description of the Study Area and Experimental Material

The study was conducted in Haro Sabu Agricultural research center of Belam sub site during the main cropping season of 2022. The average annual rainfall is 100 mm, the average annual maximum temperature is 28.40°C, and the average annual lowest temperature is 16.250°C. The experimental site's soil is a clay soil particle with Ph of 5.02.

Thirty six (36) genotypes were evaluated with the standard checks (Belete and Gudane) in 6x6 simple lattice design using 3mx1.5m plot size at the row and plant spacing of 75cm and 30cm, respectively. All agronomic data were collected and analyzed by SAS

version 9.3(SAS, 2014). the experiment consisted of 34 genotypes which were evaluated with two standard checks. Descriptions genotypes were listed below (Table 1).

2.2. Experimental Design

The experiment was laid out in 6x6 simple lattice design with two replications. Each plot was 3m x 1.5m = 4.5m²

wide, consisting of two rows, which accommodated 10 plants per row and thus 20 plants per plot. The spacing between plots and adjacent replication were 1 m and 1.5 m, respectively. The spacing between rows and plants were 70cm and 30 cm, respectively.

Table 1. Description of Experimental Materials.

S.No	Pedigree	Pedigree Code	S.No	Pedigree	Pedigree Code
1	CIP-313024. 11	G1	19	CIP-308486. 64	G35
2	CIP-313022. 202	G2	20	CIP-313039. 63	G36
3	CIP-313033 . 03	G4	21	CIP-313022. 07	G38
4	CIP-313037.13	G5	22	CIP-313022. 61	G41
5	CIP-313037.14	G6	23	CIP-313022. 65	G42
6	CIP-308538. 213	G9	24	CIP-308538. 119	G44
7	CIP-313022. 103	G11	25	CIP-313022. 153	G48
8	CIP-313033 .106	G13	26	CIP-313022. 71	G55
9	CIP-313033 . 105	G14	27	CIP-313022. 81	G58
10	CIP-313022. 15	G15	28	CIP-313038.23	G65
11	CIP-313038.45	G17	29	CIP-313022. 117	G64
12	CIP-313037.13	G18	30	CIP-313022. 173	G68
13	CIP-308486. 11	G19	31	CIP-308486. 217	G70
14	CIP-313037.109	G20	32	CIP-308486. 168	G71
15	CIP-313022. 201	G25	33	CIP-313039. 01	G73
16	CIP-308486. 10	G26	34	CIP-313039. 21	G75
17	CIP-313039. 18	G28	35	CIP-386423.13	Gudanie(variety)
18	CIP-308486. 15	G29	36	CIP-393371.58	Belete(variety)

2.3. Experimental Procedures

Land preparation: The experimental fields were cultivated by a tractor to a depth of 25-30cm. The land was leveled and ridges were made manually.

Planting: Well-sprouted, medium-sized (39-75g) tubers were planted along the edges of ridges and the depth of the planting was kept at 5 cm (Lung'aho *et al*, 2007).

Fertilizer application: NPS fertilizer was applied at the rate of 195kg ha⁻¹ and nitrogen in the form of urea was applied in split form at the rate of 165 Kg/ha (half-rate after full emergence (two

Harvesting: Potato plants were ready for harvesting when the plants achieved physiological maturity,

weeks after planting) and half-rate at tuber beginning (start of flowering)).

Crop protection: Potato plants were treated with Mancozeb 80% WP at the rate of 1.5 kg ha⁻¹ diluted at the rate of 40g per 20 litre of water once a week for three application intervals to control late blight disease. All the remaining cultural practices were carried out in accordance with regional (Haramaya University) guidelines (Teriessa, 1997).

yellowing or senescence was visible on the lower leaves, which was helpful to reduce bruising and peeling

during harvesting and post-harvest handling. For yield estimation, tubers were harvested from twenty plants which were from the two rows.

2.4. Data collection

Important phenological and yield related traits; days to maturity, tuber size, number pf tuber per hill, average tuber weight, marketable tuber yield (t ha⁻¹) and total tuber yield (t ha⁻¹) were recorded to evaluate the genotypes.

Days to maturity: It was determined as the number of days from planting time to physiological maturity.

Tuber size (cm): It was determined by measuring the tuber diameter of five tubers of different size and dividing by to get their average.

Number of tuber per hill: It was the average total number of tuber from randomly taken five plants at harvesting time.

Average tuber weight: The average tuber weight was determined by dividing the total fresh tuber yield to the respective total tubers number.

Marketable tuber yield (t/ha): All marketable tubers weighing more than 20 grams and free of pests and diseases were counted.

Unmarketable tuber yield (t/ha): The tubers that were diseased, insect attacked and small-sized (< 20 g) were recorded as unmarketable tuber yield.

Total tuber yield (t/ha): The total tuber yield weight of 20 plants per plot was recorded and converted into yield per hectare at harvest

2.5. Data Analysis

Analysis of variance (ANOVA) was used to assess the differences between genotypes on the data. Statistical Analysis System (SAS) version 9.3 software was used to compute the analysis of variance and (LSD) for treatments mean separation at 5% probability levels.

2.5.1. Estimation of Variance Component

The genotypic and phenotypic coefficients of variation were estimated using the formula suggested by [3, 31] as follows:

$$\sigma^2G = \frac{MSG - MSe}{r}$$

$$\sigma^2P = \sigma^2G + \sigma^2E$$

Where σ^2G = genotypic variance, σ^2P = phenotypic variance, σ^2E = Environmental variance, MSG = mean square of genotypes, MSe = mean square of error, and r = number of replications.

$$PCV\% = \frac{\sqrt{\sigma^2P}}{X} \times 100$$

$$GCV\% = \frac{\sqrt{\sigma^2G}}{X} \times 100$$

Where: GCV= Genotypic coefficient of variation, PCV= Phenotypic coefficient of variation, and X is grand mean of a character.

Estimation of Heritability in Broad Sense

Heritability in broad sense (h^2) of the traits were calculated according to the formula as described by Allard (1960) as follows:

$$H(h^2b) = \frac{\sigma^2g}{\sigma^2p} \times 100$$

Where: $H(h^2b)$ = Heritability in broad sense, σ^2G = Genotypic variance, σ^2P = Phenotypic variance

2.5.3. Estimation of Genetic Advance

Genetic advance (GA) was determined as described by Johnson et al. (1955)

$$GA = K \times \sigma^2P \times h^2$$

Where: K = constant (which varies depending upon the selection intensity and, 2.06 at 5% selection intensity), σp = Phenotypic standard deviation calculated as square root of phenotypic variance, h^2 = Heritability in broad sense, GA = Genetic advance.

2.5.4. The genetic advance as percentage of the mean (GAM):

According to Johnson et al. (1955) the genetic advance as percentage of the mean (GAM) was calculated as follows:

$$GAM(\%) = \frac{(GA)}{X} \times 100$$

where: GAM = genetic advance as percentage of the mean, GA= genetic advance, and X = grand mean of a character.

III. RESULT AND DISCUSSIONS

3.1. Analysis of Variance

Analysis of Variance results indicated that the genotype mean squares for most traits studied were highly

significant (Table 2). This reflected that there is high variability among 34 evaluated genotypes with two checks and this variation could be exploited in the potato yield improvement program. Many researchers

also reported statistically significant variation for various characters (Habtamu, 2023; Owusu et al, 2021; Gebrehanna et al, 2022; Workayehu et al, 2021; Zeleke et al, 2021).

Table 2. Mean squares for tuber yield and yield component traits obtained from variance analysis.

Parameters	Source of Variations			LSD(5%)	CV(%)
	Rep(1)	Genotype(35)	Error		
Days to maturity	144.5	10.26**	4.61	4.36	2.16
Tuber size(cm)	0.0089	1.88*	0.7426	1.75	5.65
Number of tuber per hill	16.63	23.43*	13.60	7.49	30.87
Average Tuber weight(kg)	0.34306806	0.06066850*	0.03846348	0.40	28.91
Marketable yield(tpha)	1047.29	78.084**	25.26	10.20	19.59
Unmarketable yield(tpha)	1.8304	0.3669	0.2219	0.96	53.39
Total yield(tpha)	1136.6117	80.927**	25.2452	10.2	18.94

In the current experiment, most of the traits exhibited wide ranges of variation between the maximum and minimum genotype mean values (Table 3). Tuber size ranged from 17.3 cm to 13 cm with mean of 15.11 whereas number of tuber per hill ranged from 19.8 to 4.90 with mean of 11.95. Marketable yield ranged from 36.85tha⁻¹ to 11.09tha⁻¹ with mean of 25.65tha⁻¹ while total tuber yield ranged from 38.65 t ha⁻¹ to 11.53tha⁻¹ with a mean of 26.53tha⁻¹

3.2. Estimates of Variance Components

According to this experiment result, genotypic variance (σ^2_g) values ranged from 0.01for average tuber yield to 27.84 for total tuber yield while phenotypic variance (σ^2_p) values ranged from 0.03 to 40.46 for average

tuber weight and total tuber yield, respectively. The GCV values were ranged from 0.04% for marketable yield to 30.60% for unmarketable tuber yield. Similarly, the PCV values ranged from 5.24% for days to maturity to 48.67 % for unmarketable tuber yield (Table 3). In the current study, the phenotypic variance was in general higher than the genotypic variance for all the characters (Table 3). Thus, it suggests the substantial influence of the environment besides the genetic variation for the expression of these traits. The same result was also reported by many authors (Gebrehanna et al, 2022, Workayehu et al, 2021).

Table 3. Genetic Variability of yield and Yield component characters evaluated for 34 potato genotypes with two standard checks

Parameters	Max	Min	Mean	σ^2_g	σ^2_p	GCV (%)	PCV (%)	Hb (%)	GA%	GAM%
Days to maturity	105.5	95.5	99.31	1.88	3.42	1.38	5.24	55.07	3.88	3.91
Tuber size	17.3	13.0	15.11	0.38	0.63	4.08	23.39	60.50	0.78	5.17
Number of tuber per hill	19.8	4.90	11.95	3.28	7.81	15.15	19.91	41.95	6.75	56.48
Average tuber weight	0.99	0.24	0.68	0.011	0.030	15.50	25.61	60.50	0.04	5.56
Marketable yield	36.85	11.09	25.65	26.41	39.04	0.04	24.36	67.65	54.40	212.10
Unmarketable yield	2.02	0.26	0.88	0.073	0.183	30.60	48.67	39.52	0.15	16.97
Total tuber yield	38.65	11.53	26.53	27.84	40.46	19.89	23.98	68.80	57.35	216.18

Characters with high estimates of GCV and PCV has a high potential for effective selection but, characters having low estimates for both variability components is complex for selection due to the masking effect of environment on the genotypic effect (Burton, 1957, Singh, 1990). According to Deshmukh *et al.* [11], PCV and GCV values greater than 20% are considered as high; values between 10% and 20% are medium; whereas values less than 10% are considered as low. In this study genotypic coefficient of variation estimates were high (>20%) for unmarketable yield. Accordingly, these traits practically provide high chance for effective selection. In contrast, total tuber yield, number of tuber per hill and average tuber weight had moderate (10-20) GCV values, those traits provide practically moderate chance for selection whereas, days to maturity, tuber size and marketable yield had low (<10) GCV values, and hence these characters provide practically less chance for selection.

3.3. Estimation of Heritability in Broad Sense and Genetic Advance

Estimates of heritability in a broad sense ranged from 39.52 for unmarketable yield to 68.80 for total tuber yield (Table 3). According to Johnson(1955), if the heritability of a character is very high, selection for such characters could be easy. This is because there would be a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype. As a result of the environment's masking effect, selection may be extremely challenging or almost impossible for traits with low heritability. Heritability (h^2 bs) values were classified as low (0-30%), moderate (30-60%) and high (>60%) (Johnson *et al.*, 1955). Considering this as standard, the heritability estimate in this study was high for tuber size, average tuber weight, marketable yield and total tuber yield, while it was moderate for days to maturity, number of tuber per hill and un marketable yield. Therefore, these characters such as tuber size, average tuber weight, marketable yield and total tuber yield are effective for selection to improve potato productivity. In line with this result, Habtamu (2023) reported the highest heritability estimates for studied traits which was ranged from 71.95% to 99.77% Which might be due to a close correspondence between the genotype and the phenotype due to the relative small contribution of the environment to the phenotype..

According to the study result, genetic advance as

percentage of mean ranged from 3.91% days to maturity to 216.18% total tuber yield. The magnitude of genetic advance as percentage of mean was categorized as low (0-10%), moderate (10- 20%), and high (> 20%), as suggested by Johanson *et al.* (1955). Accordingly high genetic advance as percentage of mean were recorded number of tuber per hill (56.48%), marketable yield (212.10%), while medium GAM were recorded for un marketable yield(16.97%); whereas, low genetic advance as percentage of mean recorded for days to maturity (3.91%), tuber size (5.17%) and average tuber weight (5.56). According to Singh (1990), high heritability estimates combined with high genetic advance are usually more useful than heritability estimates alone in forecasting gain under selection. Whereas, low heritability accompanied with genetic advance is due to non-additive gene effects for the particular character and would offer less scope for selection because of the influence of the environment. In the present study, high heritability coupled with high-expected genetic advance as percentage of mean was recorded for marketable yield and total tuber yield As a result, marketable yield and total tuber yield are critical for a breeder to consider while making a selection. The current result was in line work of Getachew *et al*, 2016 who reported high heritability estimates along with the high genetic advance for tuber yield, number of tubers and average tuber weight, and marketable tuber yield. Similarly many researchers reported related results heritability estimates along with the high genetic advance for tuber yield, number of tubers and average tuber weight, and marketable tuber yield (Wolie *et al*, 2013 and Zeleke *et al*, 2021).

IV. CONCLUSION AND RECOMMENDATION

The results of this study revealed the existence of significant variation among tested potato genotypes with two standard checks for all the examined traits. The significant variation and high range mean values indicates the presence of considerable variability in tested genotypes and two standard checks for economic importance traits and the higher chance of selecting best genotypes with high yield to improve the crop productivity through selection. Four yield related characters namely; tuber size average tuber weight, marketable yield and total with high heritability estimates could be used as good criteria for selection in the potato improvement because, these characters had

high genotypic coefficient of variation, board sense heritability estimate and genetic advance as percent of the mean.

CONFLICT OF INTEREST

The authors have no conflict of interest.

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